

410.018
ARAND et al
Serial No.: 10/009

A circular stamp with "U.S. PATENT & TRADEMARK OFFICE" around the perimeter and "O I P E" at the top.

Filed: 11/2/01
For: EPOXIDE...ORIGIN

SEQUENCE LISTING

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FURSTOSS, ROLAND

<120> EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN

<130> bml-410.018

<140> 10/009,030
<141> 2001-11-02

<150> PCT/FR00/01217
<151> 2000-05-05

<150> FR 99/05711
<151> 1999-05-05

<160> 8

<170> PatentIn Ver. 2.1

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<212> DNA
<213> *Aspergillus niger*

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<222> (1) . . (1194)

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aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96
Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
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acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
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caa gcg gat ggc cggtt ggc atc act tct gaa tgg ctg aca act atg 192
 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
 50 55 60

cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 65 70 75 80

ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
 85 90 95

cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca	336
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala	
100 105 110	
ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg	384
Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu	
115 120 125	
cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg	432
Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu	
130 135 140	
gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
145 150 155 160	
gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg	528
Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
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att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
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aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc	672
Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
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ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
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Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Pro Ile Ala	
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Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
275 280 285	
ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
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gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act	960
Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr	
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gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att		1008
Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile		
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His Lys Pro Phe Gly Phe Ser Phe Pro Lys Asp Leu Cys Pro Val		
340	345	350
cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat		1104
Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp		
355	360	365
cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg		1152
His Ala Glu Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu		
370	375	380
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Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu		
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Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg		
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80		
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His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala		
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Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu		
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145	150	155
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Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
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Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
180 185 190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
195 200 205

Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
210 215 220

Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
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245 250 255

Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
260 265 270

Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
275 280 285

Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
290 295 300

Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
305 310 315 320

Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
325 330 335

His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
340 345 350

Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
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<212> DNA
<213> Artificial Sequence

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<213> Artificial Sequence

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44

SEQUENCE LISTING

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 PROCESSES FOR OBTAINING THEM, AND THEIR USES, IN
 PARTICULAR FOR THE PREPARATION OF ENANTIOMERICALLY
 PURE MOLECULES

10 <130> EPOXSL

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<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

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Nucleotide sequence SEQ ID NO : 1

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 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
 20 25 30

40 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
 35 40 45

45 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192
 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
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50 cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 65 70 75 80

55 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
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 85 90 95

60 cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336
 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
 100 105 110

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 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
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15	atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp 180 185 190	576
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30	ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg 225 230 235 240	720
35	atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser 245 250 255	768
40	act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Pro Ile Ala 260 265 270	816
45	tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro 275 280 285	864
50	ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr 290 295 300	912
55	gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr 305 310 315 320	960
60	gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile 325 330 335	1008
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 370 375 380

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Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
 35 40 45

25 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
 50 55 60

30 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
 85 90 95

35 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
 100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
 115 120 125

40 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
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45 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
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Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
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50 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
 180 185 190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
 195 200 205

55 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
 210 215 220

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Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
245 250 255

5 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
260 265 270

Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
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Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
290 295 300

Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
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Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
325 330 335

20 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
340 345 350

Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
25 355 360 365

His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
370 375 380

Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
30 385 390 395